

comprises [the sequence His-Lys-Cys-Gly-His] a codon encoding Lys in place of the codon encoding Glu.

10. ⁴³ (Twice amended) The nucleic acid fragment of claim ~~68~~, ⁹ wherein said at least one mutation in said motif comprises [the sequence Tyr-His-Asn-Asn-Pro] a codon encoding His in place of the codon encoding Leu.

10. ²⁷ (Three Times Amended) An isolated nucleic acid fragment comprising a sequence of at least about 20 nucleotides from a *Brassicaceae* or *Helianthus* delta-15 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation [is effective for altering fatty acid composition in *Brassicaceae* or *Helianthus* seeds] renders the product of said desaturase gene non-functional and wherein said sequence includes said at least one mutation.

31. (Amended) The nucleic acid fragment of claim [30] ²⁷, wherein said at least one mutation [comprises] introduces a non-conservative amino acid substitution in said region.

32. (Twice Amended) The nucleic acid fragment of claim ³¹, wherein the wild-type amino acid sequence of said motif comprises the [wild-type amino acid] sequence His-Asp-Cys-Gly-His.

33. (Amended) The nucleic acid fragment of claim ³², wherein said at least one mutation comprises [the sequence His-Lys-Cys-Gly-His] a codon encoding Lys in place of the codon encoding Asp.

34. (Twice amended) A *Brassicaceae* or *Helianthus* plant containing a full-length coding sequence of a delta-15

fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif and wherein said mutation [confers an altered fatty acid composition in seeds of said plant] renders the product of said desaturase gene non-functional.

37. (Amended) The plant of claim 17, wherein said mutation confers a decreased level of α -linolenic acid in [said] seeds of said plant.

40. (Twice Amended) The plant of claim 37, wherein the wild-type amino acid sequence of said motif comprises the [wild-type amino acid] sequence His-Asp-Cys-Gly-His.

41. (Amended) The plant of claim 40, wherein said at least one mutation comprises [the sequence His-Lys-Cys-Gly-His] a codon encoding Lys in place of the codon encoding Asp.

44. (Twice Amended) A *Brassicaceae* or *Helianthus* plant containing:

- a) a full-length coding sequence from a delta-12 fatty acid desaturase gene having at least one mutation, said at least one delta-12 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and
- b) a full-length coding sequence from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif;
- wherein said delta-12 gene mutation and said delta-15 gene mutation [confer an altered fatty acid composition in seeds of said plant] render the products of said delta-12 desaturase gene and said delta-15 desaturase gene, respectively, non-functional.

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45. (Amended) The plant of claim ~~44~~, wherein said mutant genes confer a decreased level of α -linolenic acid in [said] seeds of said plant compared to α -linolenic acid levels in corresponding seeds lacking said mutant genes.

46. (Twice Amended) A *Brassicaceae* or *Helianthus* plant containing a full-length coding sequence of a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a Tyr-Leu-Asn-Asn-Pro amino acid motif and wherein said mutation [confers an altered fatty acid composition in seeds of said plant] renders the product of said desaturase gene non-functional.

55. (Twice Amended) A method for producing a *Brassicaceae* or *Helianthus* plant line, comprising the steps of:

- a) inducing mutagenesis in cells of a starting variety of a *Brassicaceae* or *Helianthus* species;
- (b) obtaining one or more progeny plants from said cells;
- (c) identifying at least one of said progeny plants that contains a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said delta-12 gene mutation renders the product of said delta-12 desaturase gene non-functional; and
- (d) producing said plant line from said at least one progeny plant by self-or cross-pollination, said plant line having said at least one delta-12 gene mutation.

57. (Twice Amended) The method of claim ~~55~~, further comprising the steps of:

e) inducing mutagenesis in cells of said plant line;

- f) obtaining one or more progeny plants from said plant line cells;
- g) identifying at least one of said plant line progeny plants that contains a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said delta-15 gene mutation renders the product of said delta-15 desaturase gene non-functional; and
- h) producing a second plant line from said at least one plant line progeny plant by self- or cross-pollination, said second plant line having said at least one delta-12 gene mutation and said at least one delta-15 gene mutation.

64. (Twice Amended) A method for producing a Brassicaceae or Helianthus plant line, comprising the steps of:

- a) inducing mutagenesis in cells of a starting variety of a Brassicaceae or Helianthus species;
- b) obtaining one or more progeny plants from said cells;
- c) identifying at least one of said progeny plants that contains a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said at least one mutation renders the product of said delta-15 desaturase gene non-functional; and
- d) producing said plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said delta-15 gene mutation.

65. (Amended) An isolated nucleic acid fragment comprising a sequence of at least about 20 nucleotides from a Brassicaceae or Helianthus delta-12 fatty acid desaturase gene having at least one mutation in a region of said desaturase gene

encoding a Tyr-Leu-Asn-Asn-Pro amino acid motif, wherein said at least one mutation [is effective for altering the fatty acid composition in *Brassicaceae* or *Helianthus* seeds] renders the product of said desaturase gene non-functional and wherein said sequence includes said at least one mutation.

Please add the following new claims:

del 39. ~~67~~. A method for identifying a mutation in a *Brassicaceae* or *Helianthus* plant, comprising:

- a) providing a *Brassicaceae* or *Helianthus* plant having a decreased α -linolenic acid content as compared with a corresponding control *Brassicaceae* or *Helianthus* plant; and
- b) identifying at least one mutation in a delta-15 fatty acid desaturase gene of said plant, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said mutation renders the product of said delta-15 fatty acid desaturase gene non-functional.

del 40. ~~68~~. The method of claim ~~67~~, wherein said identifying step comprises a technique selected from the group consisting of: PCR, 3SR and direct polynucleotide sequencing.

del 69. A method for identifying a mutation in a *Brassicaceae* or *Helianthus* plant, comprising:

- a) providing a *Brassicaceae* or *Helianthus* plant having an increased oleic acid content as compared with a corresponding control *Brassicaceae* or *Helianthus* plant; and
- b) identifying at least one mutation in a delta-12 fatty acid desaturase gene of said plant, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, wherein said mutation renders the